

bonds and using its lone pair electrons to accept a hydrogen bond from the neighbouring hydrazinium ion. The N(1) atom thus takes part in three hydrogen bonds, twice as the donor and once as the acceptor of the hydrogen atom. The hydrogen atom H(1) is bonded to oxygen of the sulphate ion and the N(1)–H(1)···O(4) hydrogen bond is bent with the N(1)–H(1) direction making an angle 44° whereas Cuthbert & Petch (1963) report 39°. The other hydrogen atom H(2) is bonded to nitrogen of the neighbouring NH₂ group and the N(1)–H(2) direction makes an angle of 18° with the N(1)–N(1) direction, which is more than the value of 4.5° reported by Cuthbert & Petch (1963). The hydrogen atoms of the NH₃ group are bonded to the nearest neighbouring acceptor oxygen atoms of the sulphate ion. The bonds are not collinear but bent, the angles being 123–152°.

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The Crystal Structure of β -DL-Arabinose

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The crystal structure of β -DL-arabinose (C₅H₁₀O₅) has been determined from integrated photographic intensity data by the application of a sign-correlation procedure on an IBM 1620 computer. The structure was refined by anisotropic least squares to give a final *R* value of 0.076 for 1122 reflections. The space group is *P*2₁/*c*, with *Z*=4 and unit-cell dimensions *a*=5.925 (σ =0.004), *b*=7.820 (σ =0.003), *c*=13.354 (σ =0.006) Å and β =99.45° (σ =0.06). All the hydrogen atoms were located on difference syntheses, but were not refined. It is found that the bond C(1)–O(1)H is 1.392 Å and is significantly shorter than the mean value of 1.423 Å for the other C–OH bonds. There is no significant difference between the two ring C–O distances. These observations are consistent with those from other recent structure determinations of pyranose sugars. The D and L molecules are hydrogen-bonded in pairs across the centers of symmetry and throughout the crystal structure by centrosymmetrically related chains of hydrogen bonds, each of which links molecules of the same sense. All the oxygen atoms in the structure are involved in this hydrogen-bonding scheme.

Introduction

Both D- and L-arabinose are of biological origin. L-Arabinose occurs naturally as a free sugar and is widely distributed in the combined state in plant products, usually as a furanoside. D-Arabinose is found rarely but does occur in certain plants and in the polysaccharide of tubercle bacilli. The DL material has the trivial name 'pectinose', presumably because it can be obtained from the degradation of the polysaccharides in pectin substances.

When a DL mixture crystallizes, it may do so to form a racemic structure with a centric space group. This permits, at least in principle, a more straightforward solution to the phase problem and the attainment of a better accuracy by a factor of two in the atomic parameters (Cruickshank, 1950). We have taken advantage of this in DL-arabinose, and as far as we know, this is the first example of a centrosymmetric structure determination of a free DL sugar. The crystal structure of β -L-arabinose has been determined from a refinement of two projections by Hordvik (1961).

Crystal data

DL-Arabinose crystals were obtained by slow evaporation of an aqueous solution of the compound supplied by Mann Research Laboratories, Inc. The cell parameters were measured with Cu $K\alpha$ radiation using a single-crystal orienter on a General Electric XRD-5 spectrogoniometer. The crystal density was measured at 23°C by the flotation method in a mixture of carbon tetrachloride, chloroform and bromoform.

DL-Arabinose, $C_5H_{10}O_5$. M.W. 150.13.

Monoclinic, space group $P2_1/c$, from systematic absences: $h0l$ absent for $l=2n+1$, $0k0$ absent for $k=2n+1$.

$Z=4$.

$a=5.925$ ($\sigma=0.004$) Å.

$b=7.820$ ($\sigma=0.003$).

$c=13.354$ ($\sigma=0.006$). $\beta=99.45$ ($\sigma=0.06$)°.

$D_m=1.638$ ($\sigma=0.003$) g.cm⁻³. $D_x=1.634$ g.cm⁻³.

This density is one per cent greater than that calculated from the X-ray data on the β -L form by Hordvik (1961).

Experimental

The integrated intensity data were recorded on multiple-film equi-inclination Weissenberg photographs using Cu $K\alpha$ radiation. Using approximately cylindrical crystals of diameter 0.25 and 0.27 mm, four layers about the a axis and six layers about the b axis were taken. Of the 1520 theoretically accessible reflections unrelated by symmetry, 1122 reflections were observed above the background of the film, and their intensities were estimated visually by comparison with a standard scale. No correction for absorption or extinction was applied. These data were then correlated and reduced to the structure factors with an IBM 7090 program (Shiono, 1966) which uses the procedure described by Hamilton, Rollett & Sparks (1965).

Determination of the structure

The structure factors were converted to the normalized structure factors, $|E_{hkl}|$'s (Hauptman & Karle, 1953). The phase problem was then solved directly by a sys-

tematic sign correlation procedure using an IBM 1620 program prepared by Beurskens (1963). The signs of three linearly independent reflections were arbitrarily given positive signs in order to fix the origin and twelve more reflections with large $|E|$ values were given arbitrary signs. These 15 signs were then used to generate new signs by the Sayre (1952) relationship and their dependencies were traced back so that the most probable absolute signs could be determined, using the criterion based on the probability formula of Cochran & Woolfson (1955). This procedure gave 398 signs, which when used to compute a three-dimensional E map (Karle, Hauptman, Karle & Wing, 1958), clearly revealed the structure. The first structure factor calculation gave an R value of 0.30 for all the observed reflections.

Refinement of the structure

The refinement of the positional and thermal parameters was carried out by the Busing-Martin-Levy (1962) full-matrix least-squares IBM 7090 program.

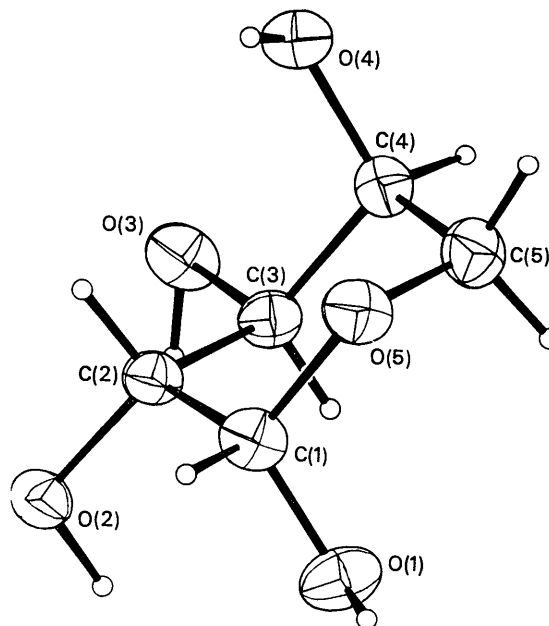


Fig. 1. Identification and numbering of the atoms in the molecule.

Table 1. Fractional atomic coordinates* in β -DL-arabinose

	x	y	z		x	y	z
C(1)	-0.0625 (5)	0.0680 (4)	0.6285 (2)	H(C1)†	0.105	0.033	0.646
C(2)	-0.1700 (5)	0.1350 (4)	0.7174 (2)	H(C2)	-0.070	0.228	0.747
C(3)	-0.4148 (5)	0.1937 (4)	0.6779 (2)	H(C3)	-0.486	0.099	0.650
C(4)	-0.4143 (5)	0.3302 (4)	0.5957 (2)	H(C4)	-0.570	0.362	0.566
C(5)	-0.2954 (6)	0.2589 (5)	0.5128 (2)	H(C5-1)	-0.380	0.168	0.477
O(1)	-0.1809 (4)	-0.0784 (3)	0.5905 (2)	H(C5-2)	-0.280	0.350	0.470
O(2)	-0.1600 (4)	0.0112 (3)	0.7956 (2)	H(O1)	-0.079	-0.120	0.555
O(3)	-0.5225 (4)	0.2610 (3)	0.7577 (2)	H(O2)	-0.280	-0.080	0.776
O(4)	-0.3139 (4)	0.4869 (3)	0.6356 (2)	H(O3)	-0.544	0.157	0.770
O(5)	-0.0668 (4)	0.2000 (3)	0.5536 (2)	H(O4)	-0.170	0.490	0.643

* The estimated standard deviations are given in parentheses and refer to the last decimal positions of respective values.

† The symbol in the parenthesis is the atom to which the hydrogen atom is bonded.

The Cruickshank (1961) weighting scheme was used and the variables included the 90 positional and thermal parameters for the carbon and oxygen atoms and one scale factor. Two cycles of isotropic refinement and two cycles of anisotropic refinement reduced R to 0.11. The difference Fourier synthesis was then examined and all the hydrogen atoms were revealed at reasonable locations with respect to the carbon and oxygen atoms.

Inclusion of the hydrogen atoms and three more cycles of anisotropic refinement gave $R=0.076$, at which stage the refinement was terminated to give positional and thermal parameters listed in Tables 1, 2 and 3. The corresponding structure factors on the absolute scale are given in Table 4. The scattering factors of Berghuis, Potters, Loopstra, MacGillavry & Veenendaal (1955) were used. The positional parameters of the hydrogen

Table 2. *Anisotropic thermal parameters* in β -DL-arabinose*

The temperature factor expression used was $\exp \{-(h^2\beta_{11} + k^2\beta_{22} + l^2\beta_{33} + 2hk\beta_{12} + 2hl\beta_{13} + 2kl\beta_{23})\}$.

	β_{11}	β_{22}	β_{33}	β_{12}	β_{13}	β_{23}
C(1)	0.0159 (9)	0.0093 (5)	0.0034 (2)	0.0010 (6)	0.0026 (3)	0.0002 (2)
C(2)	0.0148 (8)	0.0066 (5)	0.0028 (2)	0.0000 (5)	0.0013 (3)	0.0003 (2)
C(3)	0.0143 (8)	0.0075 (5)	0.0031 (2)	0.0012 (5)	0.0019 (3)	-0.0004 (2)
C(4)	0.0165 (8)	0.0089 (5)	0.0027 (2)	0.0004 (6)	0.0007 (3)	0.0002 (2)
C(5)	0.0215 (10)	0.0109 (6)	0.0028 (2)	0.0014 (6)	0.0021 (3)	0.0001 (2)
O(1)	0.0216 (7)	0.0092 (4)	0.0046 (1)	-0.0013 (4)	0.0047 (3)	-0.0015 (2)
O(2)	0.0158 (6)	0.0078 (4)	0.0030 (1)	0.0001 (4)	0.0012 (2)	0.0009 (2)
O(3)	0.0197 (7)	0.0100 (4)	0.0035 (1)	0.0044 (4)	0.0041 (2)	0.0007 (2)
O(4)	0.0171 (7)	0.0076 (4)	0.0040 (1)	-0.0001 (4)	0.0018 (2)	0.0000 (2)
O(5)	0.0186 (7)	0.0094 (4)	0.0033 (1)	0.0006 (4)	0.0034 (2)	0.0003 (2)

* The estimated standard deviations are given in parentheses, and refer to the last decimal positions of respective values.

Table 3. *Principal axes of thermal ellipsoids*

The root mean square displacement U_i corresponds to the i th principal axis of the ellipsoid and $\theta_{ia}, \theta_{ib}, \theta_{ic}$ are angles between the i th axis and the crystallographic axes a, b, c .

	i	B_i^*	U_i	θ_{ia}	θ_{ib}	θ_{ic}
C(1)	1	1.720 Å ²	0.1476 Å	146.2°	79.8°	48.7°
	2	2.215	0.1675	86.0	155.0	66.5
	3	2.694	0.1847	56.5	67.5	50.4
C(2)	1	1.570	0.1410	83.9	19.1	108.9
	2	1.919	0.1559	50.4	107.7	143.7
	3	2.062	0.1616	40.2	83.0	60.3
C(3)	1	1.478	0.1368	131.0	50.5	59.2
	2	2.088	0.1626	126.8	140.0	70.8
	3	2.279	0.1699	62.7	95.3	37.5
C(4)	1	1.827	0.1521	76.6	105.0	27.8
	2	2.186	0.1664	80.7	160.1	108.8
	3	2.328	0.1717	16.4	77.2	109.6
C(5)	1	1.815	0.1516	108.1	86.3	9.2
	2	2.519	0.1786	62.8	149.8	82.6
	3	3.089	0.1978	33.6	60.1	84.6
O(1)	1	1.755	0.1491	122.9	53.9	47.1
	2	2.247	0.1687	130.3	138.4	75.1
	3	4.051	0.2265	57.6	107.8	46.7
O(2)	1	1.621	0.1433	94.2	140.5	50.6
	2	2.155	0.1652	173.8	89.6	86.5
	3	2.349	0.1725	94.6	50.5	39.6
O(3)	1	1.372	0.1318	138.7	66.7	49.6
	2	2.155	0.1652	93.1	40.4	128.9
	3	3.718	0.2170	48.8	59.1	64.5
O(4)	1	1.863	0.1536	86.9	3.6	88.6
	2	2.279	0.1699	170.0	87.3	70.7
	3	2.817	0.1889	80.5	92.4	19.4
O(5)	1	1.615	0.1430	133.2	94.0	33.8
	2	2.274	0.1697	78.1	166.7	86.3
	3	2.993	0.1947	45.7	77.4	56.5

* $B_i = 8\pi^2 U_i^2$.

Table 4 (cont.)

1 104	114-	-8 10*	21-	-8 134	133	1 11*	16	3 42	37-	-10 22	20	7 58	53	-7 151	155-
2 125	134-	-9 29	31-	-9 58	61	2 134	145	4 12*	0	-11 55	48	8 7*	7-	-8 44	45
3 12*	2	-10 10*	9	-10 109	107-	3 62	64	5 67	70	-12 42	44	-1 71	71	-9 26	28-
4 12*	10-	-11 69	75-	-11 41	42-	4 21	17	6 12*	9	-13 8*	0	-2 149	158-	-10 33	40
5 85	86-	K= 8 H= 3		-12 35	27	5 29	31-	7 24	15-	K= 4 H= 5		-3 12*	3-	K= 5 H= 6	
6 41	41-	0 51	42-	-13 32	24	6 11*	7-	8 22	16	0 133	148-	-4 35	33-	0 10*	7-
7 42	45	1 44	42-	-14 11*	10-	7 11*	1	9 92	79-	1 58	66-	-5 12*	17	1 52	58
8 34	36	2 13*	7	-15 84	87-	8 13*	11	10 28	23	2 28	24	-6 92	75-	2 27	27-
9 10*	12-	3 12*	2	K= 2 H= 4		9 11*	12-	-1 90	91-	3 69	84	-7 37	24	3 57	71-
10 90	80-	4 80	67-	0 115	120-	10 42	40	-2 153	150	4 53	55-	-8 13*	0	4 24	31-
11 9*	8-	5 25	23-	1 160	168-	11 33	42-	-3 135	139	5 58	53	-9 12*	7	-1 59	62
12 24	30-	6 20	27	2 197	215	-1 42	44-	-4 221	207-	6 105	113	-10 20	21-	-2 65	62-
-1 45	43	7 5*	7	3 53	45	-2 149	170-	-5 57	49-	7 24	25-	-11 73	62-	-3 42	43-
-2 119	132	-1 174	156	4 253	294-	-3 129	139	-6 33	30	8 94	114-	-12 40	34-	-4 36	32
-3 34	32	-2 218	205	5 137	145	-4 93	92	-7 25	22-	9 44	56-	K= 2 H= 6		-5 61	52
-4 85	88-	-3 13*	0	6 44	41-	-5 39	38-	-8 148	145-	-1 20	18	0 115	123	-6 64	65-
-5 12*	13-	4 87	81-	7 20	20-	-6 122	121-	-9 121	118	-2 32	33-	1 25	26-	-7 18	17-
-6 61	65	-5 12*	0	8 76	75-	-7 42	41-	-10 25	22-	-3 27	25	2 9*	5-	-8 57	61
-7 247	288	-6 38	40	9 9*	8-	-8 123	129	-11 69	56-	-4 29	31	3 47	33-	K= 0 H= 7	
-8 87	92-	-7 65	57-	10 37	35	-9 77	81-	-12 21	17-	-5 26	26	4 59	50-	0 46	39
-9 29	28-	-8 51	52	11 20	19-	-10 94	104-	-13 60	50-	-6 83	86-	5 19	15	2 9*	11
-10 53	54	-9 6*	11-	12 7*	3	-11 41	35-	-14 16	15	-7 25	27-	6 32	31	4 19	23
-11 94	90-	K= 9 H= 3		-1 88	90-	-12 46	44	K= 2 H= 5		-8 23	15-	7 32	35-	-2 99	81-
-12 89	76-	0 124	115-	-2 36	34-	-13 7*	15-	0 25	27	-9 119	110-	-1 9*	10-	-4 11*	18-
-13 9*	6	1 8*	8-	-3 127	129-	-14 13	16-	1 10*	0	-10 20	13-	-2 9*	9	-6 102	90
-14 49	62	2 7*	7	-4 139	134	K= 5 H= 4		2 10*	0	-11 10*	18-	-3 70	66	-8 8*	5-
K= 6 H= 3		3 5*	30-	-5 211	222	0 177	219	3 97	102-	-12 8*	10-	-4 44	48-	K= 1 H= 7	
0 53	42	-1 36	29	-6 153	151	1 51	56	4 68	61	K= 5 H= 5		-5 36	35-	0 22	23-
1 62	57-	-2 24	19-	-7 70	71	2 38	30-	5 24	18	0 11*	4	-6 9*	0	1 10*	10
2 41	42	-3 21	20	-8 27	29-	3 46	50-	6 30	28-	1 10*	1	-7 11*	1-	2 10*	13-
3 13*	9-	-4 22	22-	-9 10*	3	4 11*	16-	7 22	19	2 89	104	-8 80	66-	3 18	36-
4 13*	26-	-5 6*	10	-10 74	66-	5 101	124-	8 24	29-	3 12*	1-	-9 29	26	4 7*	41
5 50	54	K= 0 H= 4		-11 33	29-	6 46	55-	9 57	50	4 11*	4-	-10 15	12	-1 97	89
6 40	35-	C 125	95-	-12 9*	10	7 86	77	10 29	29	5 45	40-	-11 7*	5	-2 35	35
7 29	25-	2 87	79	-13 10*	2-	8 83	84	-1 78	82-	6 9*	1-	-12 46	58-	-3 38	37-
8 30	25	4 114	104	-14 35	32	9 9*	8-	-2 75	71	7 77	87-	K= 3 H= 6		-4 36	29-
9 40	32	6 32	30-	-15 6*	8-	10 14	18-	-3 159	164	8 5*	12-	0 11*	21-	-5 29	27
10 103	105-	8 225	229	K= 3 H= 4		-1 75	75-	-4 259	284	-1 19	20	1 22	24	-6 49	45
-1 135	146-	10 23	18	0 11*	12-	-2 30	31	-5 76	80	-2 66	68-	2 41	41	-7 22	21-
-2 13*	8-	12 9*	8-	1 63	58	-3 111	121	-6 89	89-	-3 90	99	3 82	82-	-8 34	32-
-3 53	55	-2 73	63-	2 12*	16-	-4 23	19-	-7 89	87-	-4 53	51-	4 23	19	-9 35	40-
-4 141	151-	-4 103	89	3 147	173	-5 154	154	-8 39	44	-5 10*	0	5 31	33	K= 2 H= 7	
-5 89	93-	-6 52	44-	4 171	182-	-6 41	37-	-9 22	16	-6 20	19	6 9*	3	0 8*	5
-6 139	152-	-8 86	80-	5 76	76-	-7 22	22	-10 32	32-	-7 105	94-	-1 36	41	1 8*	2
-7 32	32	-10 254	259-	6 12*	10-	-8 76	73	-11 10*	1	-8 34	30	-2 28	27	2 14	14
-8 71	78	-12 144	147	7 12*	5	-9 107	119-	-12 21	15	-9 52	45	-3 57	58-	3 42	50-
-9 51	55	-14 189	154	8 11*	23	-10 29	21	-13 56	51	-10 9*	2	-4 49	48-	-1 8*	0
-10 11*	10-	K= 1 H= 4		9 13*	0	-11 28	24-	-14 30	36	-11 48	49-	-5 47	51-	-2 80	81-
-11 46	43-	0 143	142	10 31	26	-12 64	58-	K= 3 H= 5		-6 164	147	-6 164	147	-3 73	70
-12 10*	2	1 175	173	11 17	18	-13 11	13	0 12*	17	0 45	49	-7 66	61-	-4 24	21
K= 7 H= 3		2 189	199	12 6*	5	K= 0 H= 5		1 35	36-	2 80	67-	-8 59	51-	-5 8*	15-
0 130	130	3 11*	4-	-1 106	112-	0 33	25-	2 58	52	4 125	84	-9 165	154	-6 35	33
1 48	46	4 38	33	-2 61	60	2 34	37	3 35	36-	6 11*	6-	-10 44	43	-7 7*	10-
2 13*	18-	5 40	43-	-3 97	91-	4 62	59-	4 51	58-	8 7*	2	-11 33	35-	-8 49	50-
3 12*	13	6 28	10-	-4 270	290-	6 11*	9	5 114	141	-2 166	157-	K= 4 H= 6		K= 3 H= 7	
4 54	53	7 33	34	-5 151	156-	8 124	95-	6 61	73-	-4 49	37	0 48	48	0 30	32
5 11*	6-	8 21	13	-6 12*	4	10 96	83	7 52	48	-6 56	60-	1 12*	16	1 8*	5
6 26	19-	9 66	60-	-7 61	58	-2 144	129-	8 35	32	-8 128	102	2 46	47-	-1 28	31-
7 80	66	10 82	73-	-8 25	22-	-4 54	62-	9 36	39-	-10 112	92	3 18	24-	-2 91	94-
8 10*	9-	11 26	22	-9 12*	0	-6 151	142-	-1 82	79-	-12 8*	11-	4 17	15-	-3 87	98-
9 7*	2	12 9*	12-	-10 38	40	-8 192	194-	-2 90	98-	K= 1 H= 6		5 17	25-	-4 56	55
-1 50	51-	-1 198	196-	-11 11*	4	-10 168	162	-3 12*	1-	0 38	38	6 6*	21	-5 52	52
-2 50	47	-2 90	92	-12 13*	10-	-12 51	47	-4 25	24-	-1 21	16-	-1 21	15	-6 28	28
-3 65	66-	-3 87	79	-13 85	84	-14 40	40	-5 76	73	2 55	42	-2 12*	4	-7 47	55
-4 22	20-	-4 146	135	-14 9*	4-	K= 1 H= 5		-6 12*	8	3 124	112-	-3 118	111	K= 4 H= 7	
-5 22	21-	-5 11*	6	-15 19	29-	0 56	55	-7 109	119-	4 38	35	-4 12*	6-	-1 6*	51
-6 12*	9-	-6 138	120-	K= 4 H= 4		1 12*	2	-8 137	157	5 68	62	-5 29	23-	-2 7*	6
-7 35	36	-7 46	36	0 53	50	2 87	87	-9 45	50	6 55	45-	-6 20	14-	-3 27	34-

Table 5. Bond lengths and angles* in β -DL-arabinose and β -L-arabinose [in brackets]

<i>i</i>	<i>j</i>	<i>d(i, j)</i>		<i>i</i>	<i>j</i>	<i>k</i>	$\angle(ijk)$	
		β -DL	[β -L]				β -DL	[β -L]
C(1)	C(2)	1.532 (4)	Å	O(5)	C(1)	C(2)	109.5 (3)°	[109.4]°
C(2)	C(3)	1.528 (4)		O(5)	C(1)	O(1)	112.9 (3)	[113.1]
C(3)	C(4)	1.533 (4)		C(2)	C(1)	O(1)	108.3 (2)	[108.9]
C(4)	C(5)	1.515 (5)		C(1)	C(2)	C(3)	109.3 (2)	[109.2]
C(5)	O(5)	1.447 (4)		C(1)	C(2)	O(2)	111.5 (2)	[107.3]†
C(1)	O(5)	1.434 (4)		C(3)	C(2)	O(2)	112.2 (2)	[110.8]
C(1)	O(1)	1.392 (4)		C(2)	C(3)	C(4)	109.9 (2)	[109.7]
C(2)	O(2)	1.417 (4)		C(2)	C(3)	O(3)	111.7 (2)	[109.2]†
C(3)	O(3)	1.432 (4)		C(4)	C(3)	O(3)	109.4 (2)	[110.1]
C(4)	O(4)	1.425 (4)		C(3)	C(4)	C(5)	108.9 (3)	[107.1]
				C(3)	C(4)	O(4)	112.5 (3)	[111.7]
				C(5)	C(4)	O(4)	111.9 (3)	[108.3]†
				C(4)	C(5)	O(5)	111.3 (3)	[111.9]
				C(5)	O(5)	C(1)	113.4 (3)	[112.7]

* The estimated standard deviations are given in parentheses, and refer to the last decimal positions of respective values.

† These results differ in the two studies by greater than 3σ .

atoms were not refined and they were assigned the same thermal parameters as those of the carbon or oxygen atoms to which they were bonded. The thermal ellipsoid parameters given in Table 3 and illustrated in Fig. 1 show that there is no marked thermal anisotropy. Neither is there any evidence of rigid-body motion which would increase the thermal displacements of the substituent atoms relative to those of the ring.

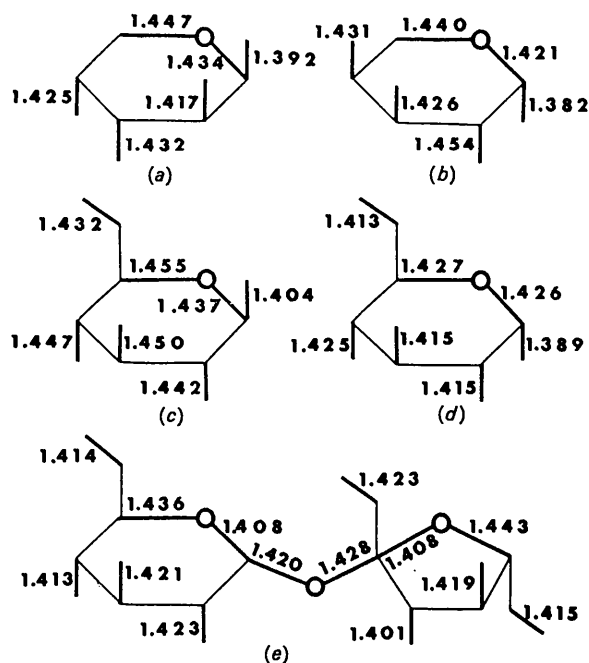


Fig. 2. C-O distance in (a) β -D,L-arabinose, (b) β -L-arabinose (c) β -D-glucose, (d) α -D-glucose, (e) sucrose.

Description of the structure

The conventional numbering and identification of the atoms for one molecule are shown in Fig. 1. The molecule is the β anomer with the chair-shaped pyranose ring. Its conformation is $1a2e3e4a$, where a and e refer to the axial and equatorial positions for the hydroxyl groups.

The bond lengths and valence angles are given in Table 5. With the exceptions discussed below, they agree within the experimental errors with those obtained by the projection analysis of the β -L-arabinose by Hordvik (1961), also shown in Table 5. The C-C bond lengths range from 1.515 to 1.533 Å and none of these differ significantly from the mean value of 1.527 Å. The C-OH bond lengths, excluding C(1)-O(1)H, range from 1.417 to 1.428 Å with the mean value of 1.423 Å. The bond length of C(1)-O(1)H is 1.392 Å and is shorter than this mean value by 7σ . This relative shortening of the C(1)-O(1)H bond length has consistently been observed in previous structure determinations of pyranose sugars with comparable values, as shown below:

β -Arabinose: 1.392 vs 1.423 Å
 $\Delta l = 7\sigma$ (this work).

β -Arabinose: 1.382 vs 1.437
 $\Delta l = 4\sigma$ (Hordvik, 1961).

α -D-Glucose: 1.389 vs 1.418
 $\Delta l = 10\sigma$ (Brown & Levy, 1965).

β -D-Glucose: 1.404 vs 1.446
 $\Delta l = 4\sigma$ (Ferrier, 1963).

α -Rhamnose: 1.376 vs 1.435
 $\Delta l = 2\sigma$ (McGeachin & Beevers, 1957)

Table 6

(a) Conformation angles in β -DL-arabinose and β -L-arabinose [in brackets].

Bond	Conformation angle*	
C(1) \rightarrow C(2)	+58.2°	[+59.9°]
C(2) \rightarrow C(3)	-57.0	[-58.4]
C(3) \rightarrow C(4)	+55.4	[+55.4]
C(4) \rightarrow C(5)	-55.8	[-55.9]
C(5) \rightarrow O(5)	+59.6	[+60.9]
O(5) \rightarrow C(1)	-60.0	[-61.3]

* The conformation angle of a directed bond C(2) \rightarrow C(3) is defined as the angle, measured clockwise, that the projection of the bond C(3)-C(4) makes with respect to the projection of the bond C(1)-C(2).

(b) Range of the conformation angles in some pyranose rings and chair form carbon rings

*Ideal value	55.8-61.7°	
Sucrose	54.8-56.0	Brown & Levy (1963)
L-Sorbose	51.6-58.2	Kim & Rosenstein (1967)
β -DL-Arabinose	55.4-60.0	Kim & Jeffrey (this paper)
β -Arabinose	55.4-61.3	Hordvik (1961)
α -D-Glucose	51.3-62.2	Brown & Levy (1965)
β -D-Glucose	52.2-66.1	Ferrier (1963)
K, Rb-Glucuronate	49.1-68.3	Gurr (1963)
† Myoinositol	53.7-59.8	Rabinowitz & Kraut (1963)
† Myoinositol . 2H ₂ O	56.0-60.1	Lomer, Miller & Beevers (1962)

* Hypothetical pyranose ring with C-C=1.525 Å, C-O(ring)=1.430 Å, valence angle on carbon atoms=109.5° and that on ring oxygen atom = 113.3°.

† Chair form six-carbon ring.

where the differences, Δl , of bond lengths between average C–OH and C(1)–O(1)H are expressed as multiples of σ 's, the estimated standard deviations of the differences.

This new result therefore adds strong support to the earlier observations and further establishes, as a general molecular characteristic of pyranose monosaccharides, that the C(1)–O(1)H link is about 0.04 Å shorter than the other C–OH. However, the fact that this shortening was not observed in sucrose (Brown & Levy, 1963) or in α -methyl-D-galactoside-6-bromohydrin (Robertson & Sheldrick, 1965) indicates that it is a property of the free hydroxyl group only. Instead, the glycosidic substituted molecules show differences in the ring C–O links, that adjacent to the glycosidic link being the shorter, a feature not observed in the presence of the O(1)H hydroxyl group. This interesting comparison between the C–O bond lengths is illustrated in Fig. 2. Unfortunately the results on cellobiose (Jacobson, Wunderlich & Lipscomb, 1961) are not sufficiently precise to be relevant. We have as yet only the one example of a mono-pyranoside substituted in the O(1) position quoted above, in which the accuracy is borderline ($\sigma=0.016$ Å) owing to the presence of the heavy atom, although the data were collected at 125°K.

The evidence for similar differences in the ring C–O bonds in furanosyl derivatives has recently been discussed by Sundaralingam (1965). There is also a trend

for the observed ring C–O links to be longer than the C–OH by about 0.01 Å, but this has yet to be established at a good significance level. The carbon valence angles inside the ring range from 108.9 to 111.3° with the mean value of 109.8° and outside the ring range from 108.3 to 112.9° with the mean value of 111.3°. The valence angle of the ring oxygen is 113.4°, *i.e.* greater than the mean values within the ring, as has been commonly observed in other structures (*cf.* Jeffrey & Rosenstein, 1964). The conformation angles of the pyranose ring are given in Table 6 and their range is compared with that of an unstrained *trans* ring and with some other pyranose and cyclohexane rings. Clearly there is no evidence of strain in the ring caused by intermolecular packing or hydrogen bonding in the crystal.

In comparing the molecular dimensions with those reported for the β -L-arabinose, one C–O distance and three C–C–OH angles have differences exceeding 3σ , as indicated in Table 5. The C(2)–O(2) distance of 1.454 Å is larger than the mean, but it remains to be established whether there is any connection between this and the fact that O(2) is involved in three hydrogen bonds in the β -L structure, rather than the more usual one or two, as in the DL form. The three angles, all of which are smaller in the β -L form, could well be the consequence of the intermolecular hydrogen bond and packing forces.

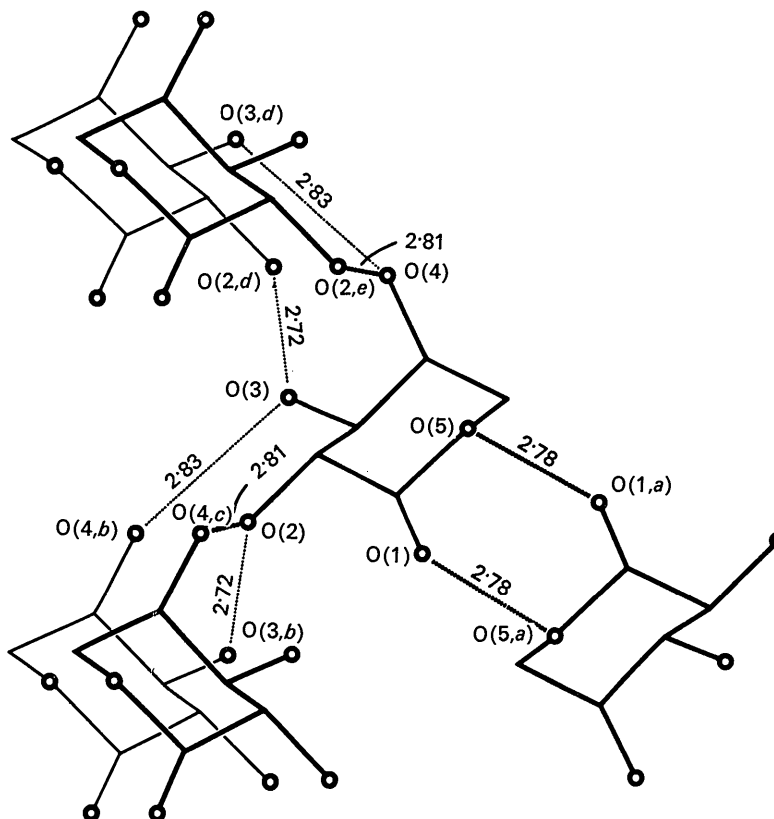


Fig. 3. Hydrogen bonding around one molecule. Dotted lines represent hydrogen bonds (See Table 7 for symmetry code).

Table 7. *Hydrogen bond distances and angles (with estimated standard deviations in parentheses)*

<i>i</i>	<i>j</i>	<i>k</i>	<i>d</i> (<i>ij</i>)	<i>d</i> (<i>jk</i>)	\angle (<i>ijk</i>)
C(1)	O(1)	O(5, <i>a</i>)		2.779 (4) Å	103.9 (2)°
C(2)	O(2)	O(3, <i>b</i>)		2.724 (3)	110.9 (2)
C(2)	O(2)	O(4, <i>c</i>)		2.809 (3)	101.7 (2)
O(3, <i>b</i>)	O(2)	O(4, <i>c</i>)	2.724 (3) Å	2.809 (3)	130.1 (2)
C(3)	O(3)	O(4, <i>b</i>)		2.834 (3)	109.2 (2)
C(3)	O(3)	O(2, <i>d</i>)		2.724 (3)	116.4 (2)
O(4, <i>b</i>)	O(3)	O(2, <i>d</i>)	2.834 (3)	2.724 (3)	113.3 (2)
C(4)	O(4)	O(2, <i>e</i>)		2.809 (3)	120.8 (2)
C(4)	O(4)	O(3, <i>d</i>)		2.834 (3)	133.0 (2)
O(2, <i>e</i>)	O(4)	O(3, <i>d</i>)	2.809 (3)	2.834 (3)	101.1 (2)

Intermolecular non-bonded distances less than 3.3 Å between carbon and oxygen atoms

<i>i</i>	<i>j</i>	<i>d</i> (<i>ij</i>)
O(5)	O(2, <i>e</i>)	3.30 Å
O(1)	O(3, <i>b</i>)	3.16

Symmetry code

—	<i>x</i>	<i>y</i>	<i>z</i>
<i>a</i>	— <i>x</i>	— <i>y</i>	1.0— <i>z</i>
<i>b</i>	—1.0— <i>x</i>	—0.5+ <i>y</i>	1.5— <i>z</i>
<i>c</i>	— <i>x</i>	—0.5+ <i>y</i>	1.5— <i>z</i>
<i>d</i>	—1.0— <i>x</i>	0.5+ <i>y</i>	1.5— <i>z</i>
<i>e</i>	— <i>x</i>	0.5+ <i>y</i>	1.5— <i>z</i>
<i>f</i>	1.0+ <i>x</i>	<i>y</i>	<i>z</i>

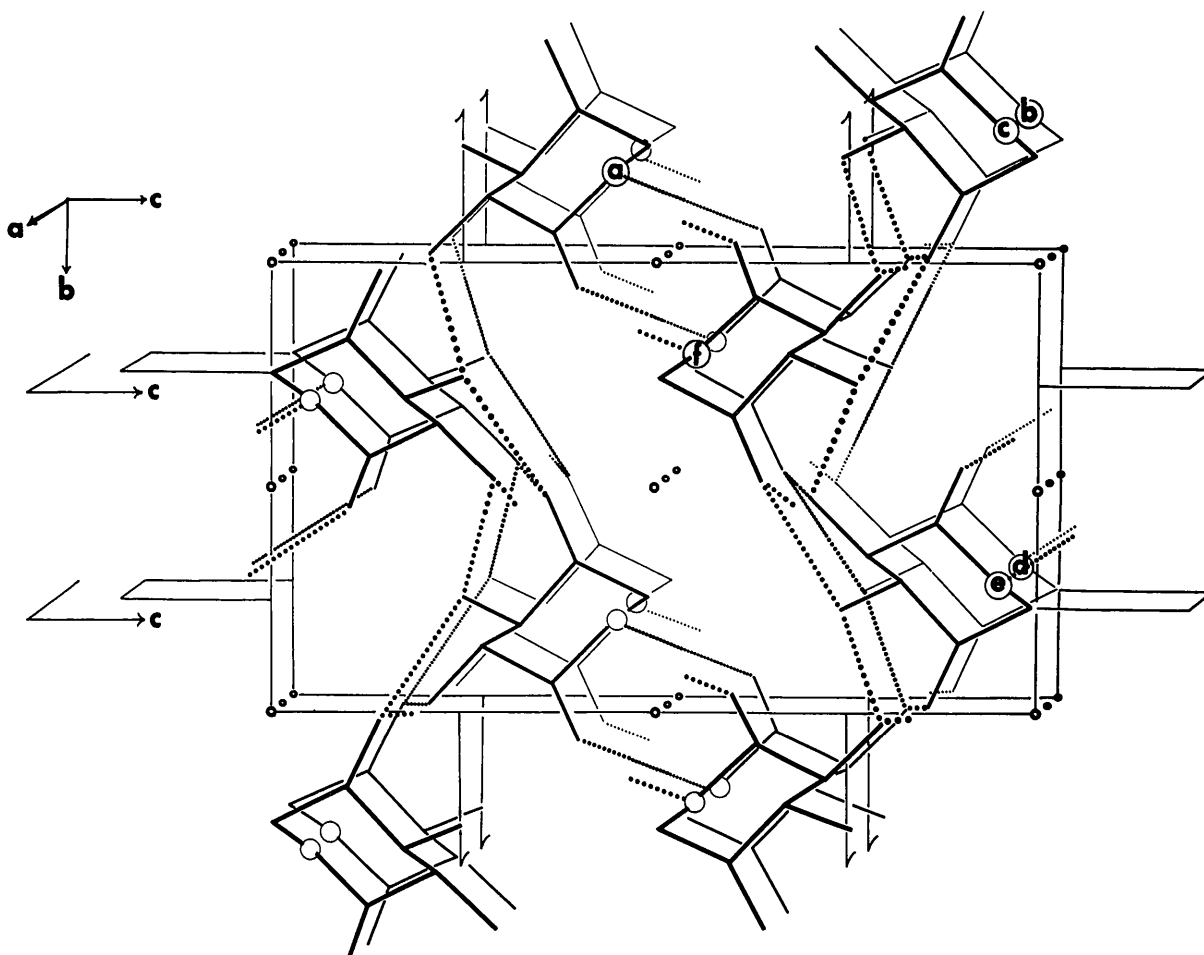
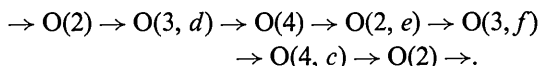


Fig. 4. Perspective drawing of the crystal structure (alphabetic symbols represent symmetry code given in Table 7).

The hydrogen bonding in the DL structure is extensive and involves all the oxygen atoms. The distances and angles are shown in Table 7. The left and right handed molecules are linked in pairs across centers of symmetry by a hydrogen bond from O(1) to O(5), the ring oxygen atom, as shown in Figs. 3 and 4. These DL pairs are then linked into a three-dimensional network by a donor/acceptor chain of hydrogen bonds which interconnect molecules of the same sense through the sequence



These hydrogen bonded chains linking a sequence of D or of L molecules are therefore also centrosymmetrically related. There are two non-bonded O...O distances which are 3.16 and 3.30 Å and these are also shown in Table 7.

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The Structure of 1,3-Diamino-2,4,6-trinitrobenzene, Form I.

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The crystal structure of 1,3-diamino-2,4,6-trinitrobenzene, form I, has been determined by X-ray diffraction. The dimensions of the monoclinic unit cell are: $a_0 = 7.30$, $b_0 = 5.20$, $c_0 = 11.63$ Å, $\beta = 95.9^\circ$. The space group is Pc with two molecules per cell. The molecule is approximately planar with apparent intramolecular hydrogen bonds between adjacent amino and nitro groups. The benzene ring is distorted so as to relieve the overcrowding of the planar configuration. The molecules are linked by intermolecular hydrogen bonds into continuous chains.

Introduction

Two crystalline polymorphs of 1,3-diamino-2,4,6-trinitrobenzene have been identified by X-ray powder dif-

fraction. Form I is stable from room temperature to 217°C and form II from 217°C to its melting point, 286°C . The solid-solid transition is rapid on heating, and the transition temperature was determined by